

Figure 1(a)

HHV8PEP	- - - - - MTPRSR-LATLGTVILLVCFCAG--AAHSRGDTFQ--
RHESRHADPEP	- - - - - MMITNRTRRLRAWVIIAIGTAVG--ENVTTPKGAT--
MURH68PEP	- - - - - MYPTVKSMRVAHLTNLLCCLCHTHLYVCQPTTLR--
BOVINEH4PEP	YYKTILFFALIKVCSFNQTTTHSTTSPLSISSTSSTTSKPSNTTNSSLAASPQ
ATELINEH3PEP	- - - - - MTLNR--CVLLIVLTFSTACS-----Q--
SAIMIRIPEP	- - - - - MVPNK--HLLLIIISFSTACG-----Q--
EQH2PEP	- - - - - MGVGGGPRVVLCLWCVAALLCQGVQAQEVVAETTPFA--
EQH5PEP	- - - - - MVAWFGLWGFARLMATLALLCGRVALDESSATPSIPP--
ALCELPEP	- - - - - MAHTGSTVCAFLIFAVLKNVFCQTPSSSEVEDVIPEAN-
EBVPEP	- - - - - MTRRRVLSVVVLLAALACRLGA----Q--TPEQ--
HHV8PEP	--TSSSPTPPGSSSKAPTPGEEASGPKSVDFYQFRVCAS-ITGELFRFNLEOTCPDTK
RHESRHADPEP	--TTAKPTP-GPS--TPTPP---ENPPR-AEAFKFRVCAS-ATGELFRFNLEKTCPGTE
MURH68PEP	--QPSDMTP-AQDAPTEPPPLSTNTNR--GFEYFRVCVGA-ATGETFRFDLDKTCPSTQ
BOVINEH4PEP	NTSTSXPSTDNQGTSTPTIPTVTDDTAS-KNFYKYRVCSASSSSGELFRFDLDQTCPDTK
ATELINEH3PEP	--TTPASSDEN--GKTPAIKEK-EYF---K-YRVCSAS-TTGELFRFNLDRAACPSTE
SAIMIRIPEP	--TTPTTAVEK--NKTQAIYQ-EYF---K-YRVCSAS-TTGELFRFDLDRTCPSTE
EQH2PEP	--THRPEVVAEE--NPANP----FLP----F--RVC GAS PTGGEIFRFPLEESCPNTE
EQH5PEP	--THKPAVHED--NTTNP----FLL----F--RVC GAS PTG-EIFRFPLEENCPNTE
ALCELPEP	--TVSDNIIRQQR--NNATAKGIHSDSA---FPFRVCAS-NIGDIFRFQTSHSCPNTK
EBVPEP	--PAPPATTVQP--TATRQ----QTS---FPFRVCELS-SHGDLFRFSSDIQCPSFG
HHV8PEP	DKY-HQEGLLVLVYKKNIVPHIFKVRRYRKIATSVTVYRGLTES--AITNKYELPRPVPLY
RHESRHADPEP	DKT-HQEGLMVFKKNIVPHIFKVRRYRKVATSVTVYRGWTET--AVTGKQEVRPVQY
MURH68PEP	DKK-HVEGLLVLVKKNIVPYIFKVRKYRKIATSVTVYRGWSQA--AVTNRDDISRAIPYN
BOVINEH4PEP	DKV-HREGILLVYKKNIVPHIFKVRRYKKIATSVRIFNGWSREGVAITNKWELSRAVPKY
ATELINEH3PEP	DKV-HKEGILLVYKKNIVPYIFKVRRYKKITTSVRIFNGWTREGVAITNKWELSRAVPKY
SAIMIRIPEP	DKD-HIEGIALIYKTNIVPYVFNRKYRKIMTSTTIYKGWSED--AITNQHTRS YAVPLY
EQH2PEP	DKE-HVEGILLIYKTNIVPYIFVNVRKYRKLVTTSTTIYKGWSQD--AITNQYTSSFAMPLW
EQH5PEP	DKE-HNEGILLIFKENIVPYVFVKRKYRKIVTTSTIYNGIYAD--AVTNQHVFSKSVPIY
ALCELPEP	TRENHTEGLLMVFKDNIIIPYSFKVRSYTKIVTNILYNGWYAD--SVTNRHEEKFSVDSY
EBVPEP	
HHV8PEP	EISHMDSTYQCFSSMKVNNGVENTFTDRDVNTTVFLQPVEGLTDNIQRYFSQPVIAE
RHESRHADPEP	EINHMDTTYQCFSSMRVNNGIVNTYTDRDFTNQTVFLQPVEGLTDNIQRYFSQPVLYTT
MURH68PEP	EVGDFDSIYQCYNSATMVVNNVRQVYVDRGVNKTVNIRPVDPGLTGNIQRYFSQPTLYSE
BOVINEH4PEP	EISMIDRTYHCFSAMATVINGILNTYIDRDSENKSVPLQPVAGLTENINRYFSQPLIYAE
ATELINEH3PEP	EINLMDKNYQCHNCMQUIEVNGLLNSYCDRGNNKTVDLKPVDGLTGAITYVSQPKIFAD
SAIMIRIPEP	EIDIMDKTYQCHNCMQUIEVNGMLNSYYDRDGNNKTVDLKPVDGLTGAITYVSQPKVFAD
EQH2PEP	EVQMMDDHYYQCFSAVQVNEGGHVNTYYDRDGWNETAFLKPADGLTSSITRYQSQPEVYAT
EQH5PEP	EARLVDNYECYNGIQTENGHTTYVDRDGYNESVRVLVPADGLTSSIRRYHSQPELYVT
ALCELPEP	ETRRMDTIIYQCYNSLDVTVGNNLLVYTDNGSNMVTDLQPVDSLNSVRRYHSQPEIHAE
EBVPEP	ETDQMDTIIYQCYNAVKMTKDGLTRVYVDRGVNITVNLKPTGGLANGVRRYASQTELYDA
HHV8PEP	PGWFPGIYRVRTTVNCEIVDMIARSAEPINYFVTSLGDTVEVSPFCYNESSCST-TPSNK
RHESRHADPEP	PGWFPGIYRVRTTVNCEIVDMIARSAEPYSYFVTALGDTVEVSPFCNDSTCSV-AEKTE
MURH68PEP	PGWMPGFIYRVRTTVNCEIVDMVARSDPYNIATALGDSLELSPFQTFDNTSQS-TAPKR
BOVINEH4PEP	PGWFPGIYRVRTTVNCEIVDMYARSVEPYTHFITALGDTIEISPFCHNNSQCTTGNSTSR
ATELINEH3PEP	AGWLWGTYKTRRTTVNCEIVEMFARSADPYTYFVTALGDTVEVSPFCDAENS CPN---AS
SAIMIRIPEP	PGWLWGTYRRTTVNCEIVDMFARSADPYTYFVTALGDTVEVSPFCVDNSCPN---AT
EQH2PEP	PRNLLWSYTTRTTVNCEVTEMSARS MKPFEFFFVTSVGD TIEMSPFLKENGTEPE--KILK
EQH5PEP	PRNLLWSYTTRTTVNCEVIDMTARSHKPFEYFVTASGDSIETSPFY-T-NASR-----R
ALCELPEP	PGWLLGGYRRRTTVNCEVTETDARAVPPFRYFITNIGDTIEMSPFWSKAWN ETEFS--GE
EBVPEP	PGWLIWTYRRTTVNCLIDMMMAKSNSPFDFVTTTQVTMSPFYDGKNKETF---HE

**Figure 1 (b)**

HHV8PEP RHESRHADPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	NGLSVQVVLNHTVVTS DRG TS PTP QNR IF VET GAY TL SWA ESK TT A C PL AL W K T F PR NGL GAR VL N Y TM V DF AT R - - A PT T ETR V FAD S G EY TV S W KA EDP K S A V C AL TL W K T F PR ADM RV REV K NY K FV D Y NN R GT A P AG Q S RT F L ETP S AT Y SW K T A T R Q T AT C DL V H W K T F PR DAT KV WIE ENH QT V D Y E R R G - H PT K DK R I F L K D E E Y T I S W K A E D R E R A I C D F V I W K T F PR DV L SS Q V DF N H T V D Y G N R AT S Q Q H G K R I F A H T L D Y S V S E A V N K S A S V C S M V F W K G F Q R D V L S V Q I D L N H T V D Y G N R AT S Q Q H K K R I F A H T L D Y S V S E A V N K S A S V C S M V F W K S F Q R R P H S I Q L L K N Y A V T K Y G V G L G Q A D N A T R F F A I F G D Y S L S W K A T T E N S S Y C D L I L W K G F S N V P - - V Q V L Y N Y S V T D Y G V G L G S G E N V T R F F A T L N D F S I S W K A A T E N S S Y C P L V L W K G F P S P D R T L T V A K D Y R V V D Y K F R G T Q P Q G H T R I F V D K E E Y T L S W A Q Q F R N I S Y C R W A H W K S F D N R A D S F H V R T N Y K I V D Y D N R G T N P Q G E R R A F L D K G T Y T L S W K L E N R - T A Y C P L Q H W Q T F D S
HHV8PEP RHESRHADPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	S I Q T T H E D S F H F V A N E I T A T F T A P - - - L T P V A N F T D T Y S C L T S D I N T T L N A S K A K L A S T H A I Q T T H E A S Y H F V A N E V T A T F T S P - - - L S E V A N F T G T Y S C L D E V I Q K T L N D T I K K L S D T H A I Q T A H E H S Y H F V A N E V T A S F L T S N Q E E T L R G N T E I L N C M N S T I N E T L E E T V K K F N K S H A I Q T E H D S T Y H F I A N E I T A G F S T S - - - K E T L A S F S S E Y S C L M S D I N S T L T D K I G R V N N T H A I Q T E H D L T Y H F I A N E I T A G F S T P - - - K E P L A N F T S D Y N C L M T H I N T T L E D K I A R V N N T H A I Q T Q H N S S L H F I A N D I T A F S T P - - - L E E E A N - F N E T F K C I W N N T Q E E I Q K K L K E V E K T H A I Q T K H E K S Y H F I A D A V T A S F T P - - - L T D E T S Y F N T T Y Q C A W Q D I E G E I Q K R F D P V S K T H A I K T E H G K S L H F V A N D I T A S F Y T P - - - N T Q T R E V L G K H V C L N N T I E S E L K S R L A K V N D T H T I A T E T G K S I H F V T D E G T S S F V T N - - - T T V G I E L P D A F K C I E E Q V N K T M H E K Y E A V Q D R Y
HHV8PEP RHESRHADPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	V P - N G T V Q Y F H T T G G L Y L V V Q P M S A I N L T H A Q - G D S G N P T S S P P P S A S P - - - - - M V T - N G S A Q Y Y K T E G G L F L L W Q P L T P L S L V D E M R G L N G - - - T T P A P - - - P - - - - - A V A - S G K T Q Y F K T D G N L Y L I W Q P L E H P E I E D I D - - E D S D P E P T P A P - - - P - - - - - K I R - D G E V K Y Y K T N G G L F L I W Q A M K P L N L S E H T - - - N - Y T I E R - - - N - - - - - N V P - N G T A Q Y F K T E G G M I L V V W Q P L T A I E L E A M I E A T T V S P T P L S - - - - - T T P - N G T A E Y Y Q T E G G M I L V V W Q P L I A I E L E A M L E A T T S P V T P S A P - - - - - T R P - N G T A K V Y K T T G N L Y I V V W Q P L I Q I D L L D T H A K L Y N L T N A T A S P T S T P - - - - - A R - N G S V Q I Y K T S G N L Y V V V W Q P L V Q L D L L A A H A K T I N S T D N S T P T A P N - - - - - T T S P - N G T A Q Y Y L T N G G L L L V W Q P L V Q Q K L L D A K G L L D A V K K Q N T T T - - - - - T T K G Q E A I T Y F I T S G G L L L A W L P L T P R S L A T V K N L T E L T P T S S P P S P P A P S A R G S T
HHV8PEP RHESRHADPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	T T S A S R R K R R S A S T A A A G G - - - G G S T D N - - - L S Y T Q L Q F A Y D K L R D G I N Q V L E E L S R A T T S T V S R V R R S V N T N E Q - - - A T D N - - - L A A P Q L Q F A Y D K L R A S I N K V L E E L S R A S T R R K R E A A D N G N S T S E V S - - - K G S E N P - - - L I T A Q I Q F A Y D K L T T S V N N V L E E L S R A K T G N K S R Q K R S V D T K T F Q G - - - A K G - - - L S T A Q V Q Y A Y D H L R T S M N H I L E E L T K T A H L T S R R T G R R K R D V S A G - - - S E N S - - - V L L A Q I Q Y A Y D K L R Q S I N N V L E E L A I T S S S R S K R A I R S I R D V S A G - - - S E N N - - - V F L S Q I Q Y A Y D K L R Q S I N N V L E E L A I T - T T S P R R R R R D T S S V S G G G - - - N N G D N S T K E E S V A A S Q V Q F A Y D N L R K S I N R V L G E L S R A T S T S S R R K R R D T G N T A T N N - - - S S S N N S S M E E N L A T S Q V Q F A Y D Q L R K S I N R V L E Q L S R V T T T R S R R Q R R S V S S G I D V - - - Y T A E S T - - - I L L T Q I Q F A Y D T L R A Q I N N V L E E L S R A P A A V L R R R R R D A G N A T T P V P P T A P G K S L G T L N N P A T V Q I Q F A Y D S L R R Q I N R M L G D L A R A
HHV8PEP RHESRHADPEP MURH68PEP BOVINEH4PEP ATELINEH3PEP SAIMIRIPEP EQH2PEP EQH5PEP ALCELPEP EBVPEP	W C R E Q V R D N L M W Y E L S K I N P T S V M T A I Y G R P V S A K F V G D A I S V T E C I N V D Q S S V N I H K S L W C R E Q V R D T Y M W Y E L S K I N P T S V M T A I Y G R P V S A K F V G D A I S V T D C V A V D Q A S V S I H K S L W C R E Q V R D T L M W Y E L S K V N P T S V M S A I Y G K P V A A R Y V G D A I S V T D C I Y V D Q S S V N I H Q S L W C R E Q K K D N L M W Y E L S K I N P V S V M A A I Y G K P V A V K A M G D A F M V S E C I N V D Q A S V N I H K S M W C R E Q V R Q T M I W Y E I A K I N P T S V M T A I Y G K P V S A K A L G D V I S V T E C I N V D Q T S V S I H K S L W C R E Q V R Q T M W Y E I A K I N P T S V M T A I Y G K P V S R K A L G D V I S V T E C I N V D Q S S V S I H K S L W C R E Q Y R A S L M W Y E L S K I N P T S V M S A I Y G R P V S A K L I G D V V S V S D C I S V D Q K S V F V H K N M W C Q N O Y R A S L M W Y E L S K I N P T S V M S A I Y G R P V S A K L V G D V V Q I S D C I T V D Q E S V F V H R N L W C R E Q H R A S L M W N E L S K I N P T S V M S S I Y G R P V S A K R I G D V I S V S H C V V V D Q D S V S L H R S M W C L E Q K R Q N M V L R E L T K I N P T T V M S S I Y G K A V A A K R I G D V I S V S Q C V P V N Q A T V T L R K S M

**Figure 1(c)**

HHV8PEP	RTN --- SKDVCYARPLVTFKFLNSSNLFTGQLGARNEIILTNQVETCKDTCEHYFITRN
RHESRHADPEP	RTS --- TPGMCYSRPPVTFRFLNSTTLFKGQLGPRNEIILTDNQVEACKETCEHYFIASN
MURH68PEP	RLQH --- DKTTCYSRPRVTFKFINSTDPLTGQLGPRKEIILSNTNIETCKDESEHYFIVGE
BOVINEH4PEP	RTD --- DPKVCSRPLVTFKFVNSTATFRGQLGTRNEIILTNTHVTCRPTADHYFFVKN
ATELINEH3PEP	KTT --- NNDVCYSRPPVTFKFVNSSLSQLFKGQLGARNEIILSESILVENCHQNAEHTAKN
SAIMIRIPEP	KTE --- NNDICYSRPPVTFKFVNSSLSQLFKGQLGARNEIILSESILVENCHQNAEHTAKN
EQH2PEP	KVPG --- KEDLCYTRPVVGFKFINGSELFAGQLGPRNEIVLSTSQVEVCQHSCEHYFQAGN
EQH5PEP.	RVPG --- SKDLCYTRPVVGFKFINGSELFVGQLGARNEIILSTNLVEVCQHSCEHYFQGGN
ALCELPEP	RVPGRDKTHECYSRPPVTFKFINDSHLYKGQLGVNNIEILTTTAVEICHENTEHYFQGGN
EBVPEP	RVPG --- SETMCYSRPLVSFSFINDTKTYEGQLGTDNEIFLTKKMTEVCQATSQYYFQSGN
HHV8PEP	ETLVYKDYAYLRTINTTDISTLNNTFIALNLSFIQNIKFKAIELYSSAEKRLASSVF <del>LET</del>
RHESRHADPEP	VTYYYKDYVFVKKINTSEISTLGTFIALNLSFIENIDFRVIELYSRAEKKLGSV <del>FDIET</del>
MURH68PEP	YIYYYKNYIIFEELNLSSIATLDTFIALNLSFIENIDFKTVELYSSTERKLASSVF <del>DIES</del>
BOVINEH4PEP	MTHYFKDYKFVKTMDTNNISTLDTFLTLNLTFIENIDFKTVELYSSTERKLASSVF <del>DIES</del>
ATELINEH3PEP	ETYHFKNYLHVETLPLTNISTLDTFLALNLTFIENIDFKTVELYSSTERKLAN - VF <del>LET</del>
SAIMIRIPEP	ETYHFKNYVHVETLPVNINSTLDTFLALNLTFIENIDFKTVELYSSTERKLAN - VF <del>LET</del>
EQH2PEP	QMYKYKDYYVSTLNLTDIPTLHTMITLNLSLIVENIDFKVIELYSKTEKRLSN - VF <del>DIET</del>
EQH5PEP	HIYKYKNYEVSTMNLTDVPTLHTMITLNLSLIVENIDFQVIELYSREEKRMST - AF <del>DIET</del>
ALCELPEP	NMYFYKNYRHVKTMPVGDVATLDTFMVLNLTVENIDFQVIELYSREEKRMST - AF <del>DIET</del>
EBVPEP	EIHVYNDYHFKTIELDGIATLQTFISLNTSLIENIDFASLELYSRDEQRASN - VF <del>LEG</del>
HHV8PEP	<b>MFREYNYYTHRLLAGLREDLDNTIDMNKERFVRDLSEIADLGIGKTVVNVASSVUTLCG</b>
RHESRHADPEP	<b>MFREYNYYTQRLAGLREDLDNTIDLNDRDLARDLSEIADLGDVGRVVNVASSVITLFG</b>
MURH68PEP	<b>MFREYNYYTSLAGIKKDDNTIDYNRDRLVQDLSMDMMADLGDIGRSVVNVSSVUTFFS</b>
BOVINEH4PEP	<b>MFREYNYYTQKLASLREDLDNTIDLNDRDLVKDLSEMMADLGDIGKVVNTFSGIVTVFG</b>
ATELINEH3PEP	<b>MFREYNYYAQOSISGLRKDFDNSQRNNRDRIIQDFSEIILADLGSIGKVIVNIASSAFSLFG</b>
SAIMIRIPEP	<b>MFREYNYYAQOSISGLRKDFDNSQRNNRDRIIQDFSEIILADLGSIGKVIVNVASGAFSLFG</b>
EQH2PEP	<b>MFREYNYYTQNLNLGRKDDDSIDHGRDSFIQTLGDIQMDLGTIGKVVNVASGVFSLFG</b>
EQH5PEP	<b>MFREYNYYTQNLKGLRKDDDSIDHGRDSFIQFLGDLVQDLPVGDVIVNVASGVFSLFG</b>
ALCELPEP	<b>MFREYNYYTQRVVTGLRRDLTD-LATNRQFVDAFGSLMDDLGVVGKTVLNAVSSVATLFS</b>
EBVPEP	<b>IFREYNFOAQNIAGLRKDDDNAVSNGRNQFDGLGELMDSLGSVGQSITNLVSTVGGLFS</b>
HHV8PEP	SLVTGFINFIFKHPLGGMLMIIIVIAIIILIFMLSRRNTIAQAPVKMIYP---DVDRRA
RHESRHADPEP	SIVSGFINFIKSPFGGMLMILVIVAVVLLIVFALNRRNTAIAQAPIRMIYP---DIDKMQ
MURH68PEP	SIVTGFIFKFFTNPLGGIFILLIIGGIIFLVVVLNRRNSQHDAPIKMLYPSVENYAARQA
BOVINEH4PEP	SIVGGFVSFFTNPIGGVTIILLIIVVVFVVIVSRRRTNNMNEAPIKMIYP---NIDKAS
ATELINEH3PEP	GIVTGINFIKNPLGGMLTFLLVGAIILVILLVRRRTNNMSQAPIRMIYP---DIEKSR
SAIMIRIPEP	GIVTGINFIKNPLGGMFTFLLIGAVIILVILLVRRRTNNMSQAPIRMIYP---DVEKSK
EQH2PEP	SIVSGVISFFKNPFGGMILLIVLIIAGVVVYLFMTRSRSIYSAPIRMLYP---GVERAA
EQH5PEP	SIVSGVISFLKNPLGAILTIALIVGGIIVLYLFITRSRTVYQAPIRMLYP---EVDRAP
ALCELPEP	SIVSGIINFIFKNPFGGMILFGLIAAVVITVILLNRKAKRFAQNPVQMIYP---DIKTIT
EBVPEP	SLVSGFISFFKNPFGGMILLVLVAGVVILVISLRRTRQMSQQPVQMLYP---GIDELA
HHV8PEP	PP ----- SGGAPTREEIKNILLGMHQLQQ --- ERQKADDLKSTPSVFQRTANGLR
RHESRHADPEP	P ----- SGGKVDQEIQIKNILAGMHQLQQ --- EERRRLDEQQRSAPSIFRASDGLK
MURH68PEP	PPPSA --- SPPAIDKEEIKRILLGMHQVHQ --- EEKEAQKQLTNQGPTLWQKATGFLR
BOVINEH4PEP	EQE ----- NIQPLPGEETIKRILLGMHQLQQ --- SEHGKSEEEASHKPGLFQLLGDLQ
ATELINEH3PEP	S ----- SVTPTEPEVIKQILLGMHNMQQ --- EYKKREEHKASQPSFLKRATDAFL
SAIMIRIPEP	S ----- TVTPMEPETIKQILLGMHNMQQ --- EAYKKKEEQRARPSIFRQAAETFL
EQH2PEP	QEP ----- GAHPVSEDQIRNILMGMHQFQQRQRAEEARREEEVKGKRTLFEVIRDSAT
EQH5PEP	QQ ----- NVQPIPEDQVRSILLAMHQFQQQQQQQQQQEEHTQ - RRSIFDTIRESTS
ALCELPEP	SQREEL --- QVDPISKHELDRLIMLAMHDYHASK -- QPESKQDDEEQGSTTSGPADWLNAK
EBVPEP	QQHASGEGPGINPISKTELQAIMLALHEQNQ --- EQKRAAQRAAGPSVASRALQAAR

Figure 2

ATGGCAGGTA GCTTAAAAC TAGGGGATCT GTTCTAGCAC TGTGGTACCT GTATCAGGTG 60  
GCTCTTTATT CACTTAGTAT AGCAGAGACC GGTGTAACCT CACCTCCAAA TACAGCGACC 120  
TGGTCTACTG AATCGCCGCT AACAGGTACAC TATGGAACAC ACGATTCAG CCATGGTGAA 180  
AGAGGAAACAA ACGAAAACAG AGATTCAAGA GAGCAAATA AAAACATTTA TGATCGCCT 240  
TCTACGTTTC CTTACAGAGT ATGCAGTGCC TCCGGAGTTG GAGATGTCTT TAGATTCAG 300  
ACCGACCATG TGTGTCGGAG TGCCAGTGAT ATGGTACACA GTGAGGGGAT TCTACTAATT 360  
TACAAACAGA ACATTATTCC ATTTATGTT AGAGTTAGGA AATATAGAAA AGTTGTTACA 420  
ACAAGTACTG TCTACAATGG TATTTATTCT GACTCTATTA CCAACCAACA TACTTTCTAT 480  
AAATCAATCG AACCTGGGA GACAGAAAAG ATGGACACAA TATATCAGTG TTTAATTCT 540  
TTAAGACTAA ACACAGGTGG AAATCTGCTT ACTTATGTAG ATAGAGATGA TATAAATATG 600  
ACAGTGTTC TGCAACCTGT TGACGGTGTG ACGCCCGATG TGAAGAGGT TGGCAGTCAA 660  
CCAGAGCTGT ACCTTGAACC TGGCTGGTT TGGGTAGTT ATAGAAGACG AACTACAGTG 720  
AACTGTGAAC TAATGGACAT GTTTCAAGA TCAAATCCTC CATTGATTT CTTGTTACA 780  
GCTACAGGTG ATACGGTGG AATGTCTCCA TTTTGGAGTG GTGAAGATGA TCATGAAAAT 840  
AAGATGCAG AGAACCATG GTTTGTAGT GTGATAAATA ACTACAAGGT GGTGGACTAT 900  
CAAAACAGAG GGACTGTACC CCTTGGAAAA ACAAGGATAT TTCTAGATAG GGAAGAGTAT 960  
ACATTATCTT GGGAAAAGCA TCTAAAAAAAT ATGTCATATT GTCCACTAAC ATTATGGAAA 1020  
GCATTTTACA ATGGAATCCA GACGGAGCAT TCAGGCTCAT ATCATTGTTGT AGCCAATGAC 1080  
ATCACAGCGT CATTCAACAC TAGTAAAGAA GACATGAAAG AGTTCAATAC GACATATCAT 1140  
TGTCTCAACG AGGAAATAAA GGCAGAAATA GAGAAGAAAT ATGCAAAAGT AACTCAACT 1200  
CACTCTAAAT ATGGAGATCT GAAATACCTT AAAACAGATG GGGGTCTCTA TTAGTCTGG 1260  
CAACCTCTTAA TTCAAAACAG GCTTCTTGAT GCTAAGAACAA AACTGAACAA TGAGACTTAT 1320  
TCCAGGAGAT CACGACGTCA GGCAGAATCT ACTACTGACC CAATGATGGA GATGACTGGA 1380  
AATGGGACAG GTGGAGAATA TAGCAGTGAA ATTCAATCA CGGTGGCGCA GGTGCAGTAT 1440  
GCCTATGACA ATCTTCGTAT CAGAATAAT AACATTTGG AAGATTGTC AAAGGCATGG 1500  
TGTCTGAGC AGCATAGAGC TGCTCTGGTG TGGATGAGC TCAGCAAGAT TAATCCCACA 1560  
ACCGTCATGA GCATGATTAA CAATAGACCC GTATCAGCCA AAAGAATAGG AGATGTCATT 1620  
TCAGTCTCTA ACTGTATTGT GGTAGACCAA ACCAGTGTCT CATTACATAA AAGTCTCAGG 1680  
CTTCTCAGTG CATCGGATGA AAAGTCTTC TCTAGACCTC CAGTGACATT TAAGTTTATG 1740  
AATGACAGTA CTATTACAA AGGGCAACTA GGAGTCAATA ATGAGATTCT CTTAACACACA 1800  
ACATACCTTG AAACATGTCA GGAAAACACT GAGTATTACT TTCAGGCAAA GACAGACATG 1860  
TACATTTACA AAAACTATGA GCATTTGAAG ACTGTGCCTT TATCTTCGAT CACCACACTA 1920  
GATACATTAA TAGCCCTTAA TTTTACACTA TTGGAGAATG TTGACTTTAA AGTCATTGAA 1980  
CTTTATACCA GGGACGAGAA GAGGCTTAGT AATGTCCTTG ACATTGAAAC AATGTTAGG 2040  
GAATATAACT ACTATGCTCA GAGGGTCAGT GGCCTCAGAA AGGATTGCT GGATCTAAC 2100  
ACCAATAGAA ATCAATTGT GGATGCATT GGTAGTCTTA TGGATGATTT GGGTGCTGTT 2160  
GGGCAGACAG TTGTAATGC TGTAAGTGGT GTGGCTACGC TGTTTAGCTC AATTGTAACA 2220  
GGATTTATTA ATTTCACTAA AAACCCATTG GGTGGAATGT TAATGATTAT TGTTGTTATT 2280  
GGTGTGCTAT TTGCCATCTA CTTTCTGACC AAAAAGACGA AGATATATGA GACGGCACCG 2340  
ATTAAGATGA TTTATCCTGA AATTGACAAG CTGAAAGAAC GTGAGGGAAA ATCAGAAATA 2400  
GCACCAATCA GTGAAGAAGA GCTGGAGAGA ATTGTACTTG CTATGCACAT CCATCAACAA 2460  
AATTCAACATA TGGAAACAAA AACAAAGGAAG GATCCCAAAG ACAGCATATT AACAAAGGGCA 2520  
CAAAATATGC TACGAAAG ATCAGGATAT TCTAATTAA AAAATGCTGA ATCTGTGGAG 2580  
ATGTTAAACA CTTTATAA 2598

**Figure 3**

MAGSLKLRRGS	VIALWLYQV	ALYSLSIAET	GVTSPPTNTAT	WSTESPLTGH	500
YGTHDSSHGE	RGNNENRDSE	EQNKNIYGSP	STFPYRVCSA	SGVGDVFRFQ	100
TDHVCPDASD	MVHSEGILLI	YKQNIIPFMF	RVRKYRKVVT	TSTVYNGIYS	150
DSITNQHTFY	KSIEPWETEK	MDTIYQCFNS	LRLNTGGNLL	TYVDRDDINM	200
TVFLQPVDGV	TPDVKRYGSQ	PELYLEPGWF	WGSYRRRTV	NCELMDFAR	250
SNPPFDFFVT	ATGDTVEMSP	FWSGEDDHEN	KMHEKPWFVS	VINNYKVVDY	300
QNRGTVPLGK	TRIFLDREEY	TLSWEKHLKN	MSYCPLTLWK	AFYNGIQTEH	350
SGSYHFVAND	ITASFTTSKE	DMKEFNTTYH	CLNEEIKAEI	EKKYAKVNST	400
HSKYGDLYKF	KTDGGGLYLVW	QPLIQNRLLD	AKNKLNNETY	SRRSRRQAES	450
TTDPMMEMTG	NGAGGEYSSE	NSITVAQVQY	AYDNLRIRIN	NILEDLSKAW	500
CREQHRAALV	WNELSKINPT	SVMMSIYNRP	VSAKRIGDVI	SVSNCIVVDQ	550
TSVSLHKSLR	LLSASDEKCF	SRPPVTFKFM	NDSTIYKGQL	GVNNEILLTT	600
TYLETQCENT	EYYFQAKTDM	YIYKNYEHLK	TVPLSSITTL	DTFIALNFTL	650
LENVDFKVIE	LYTRDEKRLS	NVFDIETMFR	EYNYYAQRVS	GLRKDLDLDS	700
TN RNQFVDAF	GSLMDDLGA V	GQTVVNAVSG	VATLFSSIVT	GFINFIFKNPF	750
GGMLMIIVVI	GVLFAIYFLT	KKTKIYETAP	IKMIYPEIDK	LKEREKGKSEI	800
APISEEELER	IVLAMHIHQO	NSHMETKTRK	DPKDSILTRA	QNMLRKRSGY	850
SNLKNAESVE	MLNTL				865

**Figure 4**

pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	AATCT TCGTATCAGA ATAAATAACA CGCCGCCGTC CGGCTCCACG GTGGTGCAGC GCAGGC--CT T G C GA A . C.	25 688
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	TTTTGGAAAGA TTTGTCAAAG GCATGGTGTC GTGAGCACGA TAGAGCTGCT GCCCGAGTA CTCG-CAGGG GCGCAACTTC ACGGAGGGGA TCGCCGTGCT GA A T G CA G GC TC G . G A T G TGCT	75 737
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	CTGGTGTGGA ATGAGCTAG CAAGATTAAT CCCACAAGCG TCATGAGCAT CT---T-CA AGGAGAACAT C--G-CC--C CGCACAAGT- TCAAGGCCA CT T A A GAG CA C G C ACAAG TCA G . C	125 776
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	GATTTACAAT -AGACCCGTA TCAGC-AAA AGAATAG-GA GATGTCATT CATCTACTAC AAGAACGTCA TCGTCACGAC CGTGTGGTCC GGGAGCACGT AT TAC A AGA C A TC C C A G T G G CA T	172 826
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	CAGTCTCTAA C-TGTATTG- -TGGTAGACC AAACCAGTGT CTCATTACAT ACGGGGCCAT CACCAACCGC TTCACAGACC GCGTGGCCGT CCCCCTGCAG G C A C G A G T AGACC GT C C T CA	219 876
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	AAAAGTCTCA GGCTTCTCGAG TGCATCGGAT GAAAAGTGT TCTCTAGACC GAGA-TCACG GACGTGATCG ACCGCCG--C GGCAAGTGC GTCCTCA-AGG A A T C C C T G C CG G AAGTGC TCTC A A	269 922
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	TCCAGTGACA T--TTAA-GT TTATGA-ATG ACAGTACT-A TTTACAAAGG CCGAGT-ACG TGGCAACAA CCACAAGGTG ACCGCCTTCG ACCGGGACGA C AGT AC T AA A A TG AC G T C AG	314 971
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	GCAACTAG-- GAGTCATAA TGAGATTCT- ---CTTAAC ---CACAACA GAACCCCGTC GAGGTGGACC TGCGCCCCTC GCGCCTGAAC GCGCTCGCA G A C GAG TG G CT CT AAC C C	354 1021
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	TAC-C--TTG AAACA-TGTC -AGGAAA--- ACACTGAGTA TTAC-TTTC CCCGGGCTG GCACACCACC AACGACACCT ACACCAAGAT CGGGGCCGCG C C TG ACA C A GA A ACAC AG C C	395 1071
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	GGCAAAGACA GACATGTACA TTTACAAAAA CT--AT--- GAGCATTG GGCTTCTAC- CACACGGCA CCTCCGTCAA CTGCATCGTC GAGGAGGTGG GGC AC ACA G CA T C AA CT AT GAG A TG	439 1120
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	AGAC----- TGTGCCTT TA----- TCT TCGATCACCA CACTAGATAC AGGCGCGCTC CGTGTACCCC TACGACTCCT TCGCCCTGTC CACGGGGAC AG C TGT CC TA CT TCG C CAC G AC	476 1170
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	ATT---TATA GCCCTTAATT TTAC--ACTA TTGGAGAATG TTGACTTTAA ATTGTGTACA TGTCCTCTT CTACGGCTG CGCGAGGGG CCCACGGGG ATT TA A C TT TAC T GAG G AC A	521 1220
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	AGTCATGTGAA CTTTATACCA GGG----ACG AG-AAGAGGC TTAGTA--AT GCACATCG-G CTACCGGCC GGGCGCTTC AGCAGGTGGA GCACTACTAC CAT G CT CC GGG C AG G GG A TA A	564 1269
pGHV-gpB DNA.txt pGHV1 DNA. (641-1300)	GTCTTGACA TTGAAACAAT G----- 585 CCCATCGAC- CTGGACTCGC GCCTCCGCC CT 1300 C T GAC TG A G	

**Figure 5**

pGHV-gpB prot PGHV1Prot. (491-850)	-----N LRI----- PAAPAAARRA RRSPGPAGTP EPPAVNGTGH LRITTGSAEF ARLQFTYDHI LRI	4 540
pGHV-gpB prot PGHV1Prot. (491-850)	--RINNILED LSKAWCREQH RAALVWNELS KINPTSVMSM IYNRPVSAKR QAHVNDMLGR IAAACELQN KDRTLWSEMS RLNPNSAVATA ALGQRVSARM N L AWC Q W E S NP V VSA	52 590
pGHV-gpB prot PGHV1Prot. (491-850)	IGDVISVSN C IVVDQTSVSL HKSLRLLSAS DEKCFSRPPV TFKFMNDSTI LGDVMAISRC VEV-RGGVYV QNSMR-VPGE RGTCYSRPLV TFE-HNGTGV GDV S C V V S R C SRP V TF N	102 637
pGHV-gpB prot PGHV1Prot. (491-850)	YKGQLGVNNE ILLTTTYLET CQENTEYYFQ AKTDMYIYKN YEHLKTVPLS IEGQLGDDNE LLISRDLIEP CTGNHRRYFK LGSGYVYYED YNYVRMVEVP GQLG NE L E C N YF Y Y V	152 687
pGHV-gpB prot PGHV1Prot. (491-850)	SITTLDTFIA LNFTLLENVD FKVIELYTRD E-----KR----- --ETISTRVT LNLTLLLEDRE FLPLEVYTR E LADTGLLDY SEIQRRNQLH T LN TLLE F E YTR E R	185 735
pGHV-gpB prot PGHV1Prot. (491-850)	----- ALKFYDIDRV VKVDHNVVLL RGIANFFQGL GDVGAAVGKV VLGATGAVIS	185 785
pGHV-gpB prot PGHV1Prot. (491-850)	-----LS NVF----- AVGGMVSFLS NPFGALAIGL LVLAGLVAAF LAYRHISRLR RNPMKALYPV LS N F	190 835
pGHV-gpB prot PGHV1Prot. (491-850)	-----DI E--TM----- TTKTLKEDGV DEGDV 195 850	

**Figure 6**

pGHV-gpB DNA.txt pGHV2 DNA.txt	CCAGCATAAT GATAGCCAAT AATCTGTGTT ACTCTACCCT GATCTTAAAT	50
pGHV-gpB DNA.txt pGHV2 DNA.txt	GACGAGGACG TGACGGGGAT CGACGAGAAA GATATTCTGA CGGTGCATGT AT T	5 100
pGHV-gpB DNA.txt pGHV2 DNA.txt	TCGTATCAGA ATA-AAT-AA CATTGGAA GATTTGCAA AGGCATGGTG -AAACAAGA ATACCGTGTGTA CAGGTCG-T TAGGAG-CAG CGTCAGGGAG A AGA ATA T A CA TT G A G CA G CA GG G	53 146
pGHV-gpB DNA.txt pGHV2 DNA.txt	TC-GTGAGCA GCATAGAGCT GCTCTGGTGT GGAATGAGCT CAGCAAGATT TCTATACTCG GCAC---GCT GCT---GTCT AG-ATG-GCT CAGGAAGAGA TC T C GCA GCT GCT GT T G ATG GCT CAG AAGA	102 188
pGHV-gpB DNA.txt pGHV2 DNA.txt	AATCCCACAA GCG-TCATGA GCATGATTTA CAAT-AGACC CGTAT-CAGC AA---GGAA GTGAAGGCAGC GCATGAAACG CTGTGAGGAC CCTATGTTGG AA AA G G G GCATGA C T AG C C TAT T	149 234
pGHV-gpB DNA.txt pGHV2 DNA.txt	CAAAAGATA GGAGATGTCA TTTCAGTCTC TAACTGTATT GTGGTAGACC C-ACTG-AT- -ACTTGACA -AGCAGCAGC TTGC--CCTC AAGGT-GAC- C A G AT A TG CA CAG C T C T GGT GAC	199 274
pGHV-gpB DNA.txt pGHV2 DNA.txt	AAACCACTGT CTCATTACAT AAAAGTCTCA GGCTTCTCAG TGCATCGGAT -GTGCAATGC GTT-TTAC- -GGCTCA CGGGAGCC-G TGCA-CGG-T CA TG T TTAC G TCA G C G TGCA CGG T	249 314
pGHV-gpB DNA.txt pGHV2 DNA.txt	GAAAAGTGCT TCTCTAGACC TCCAGTGACA TTTAAGTTTA TGAATGACAG CTGCTGC-CG TGTCT--CCC TCTAGCGCG TCCA---TCA CCAGC-ATAG G C T TCT CC TC AG G C T A T A A A AG	299 357
pGHV-gpB DNA.txt pGHV2 DNA.txt	TACTATTTCAC AAAGGGCAAC TAGGAGTCAA TAATGAGATT CTCTAACCA GGC---GGGAC A---TGC--T TAGG---CA- -GACGAG-TG ACTTTATCAA C AC A GC TAGG CA A GAG T TTA C A	349 394
pGHV-gpB DNA.txt pGHV2 DNA.txt	CAACATACCT TGAAACATGT CAGGAAACCA CTGAGTATTA CTTTCAGGCC CAATGT-CCT T-----TCGT CTAGAGAATA CG----- CAA T CCT T GT C GA AA A C	399 420
pGHV-gpB DNA.txt pGHV2 DNA.txt	AAGACAGACA TGTACATTTA CAAAAACTAT GAGCATTGAGA AGACTGTGCC	449 420
pGHV-gpB DNA.txt pGHV2 DNA.txt	TTTATCTTCG ATCACCAACAC TAGATACATT TATAGCCCTT AATTTTACAC	499 420
pGHV-gpB DNA.txt pGHV2 DNA.txt	TATTGGAGAA TGTGACTTT AAAGTCATTG AACTTTATAC CAGGGACGAG	549 420
pGHV-gpB DNA.txt pGHV2 DNA.txt	AAGAGGCTTA GTAATGTCTT TGACATTGAA ACAATG	585 420

**Figure 7**

pGHV-gpB prot	NLRIRINNIL EDLSKAWCRES QHRAALVWNE LSKINPTSVMSMIYNRPVSA	50
pGHV2 prot.txt	S--IMIANNL -----C---YSTLI---LNDEDVTG-----IDE	25
	I I N L C S L L T	
pGHV-gpB prot	KRIGDVISVS NCIVVDQTSV SLHKSLLRS ASDEKCFSRP PVTFKFMNDS	100
pGHV2 prot.txt	K---DILTVH ---VNKNTV-----YRFVRSS	45
	K D V V V F S	
pGHV-gpB prot	---TIYKGQL GV-NNBILLT TTYLSTCOQN TEYYFQAKTD MYI---YKN-	142
pGHV2 prot.txt	VRESILGTLL SRWLRKRKEV KARMKRCEDP MLALILDQQ LALKVTCNAF	95
	I L C K	
pGHV-gpB prot	YEHLKTVP-- LSSITTLDTF IALNFTLL-E NVDFKVIELY TRD---EK-R	185
pGHV2 prot.txt	Y GFTGAVHGL LPCLPLAASI TSIGRDLRQ TSDFINNVLS SREYVSEKFS	145
	Y V L L DF R EK	
pGHV-gpB prot	LSNV-F--DI ETM-	195
pGHV2 prot.txt	LSDGDFQGDF SPEC	159
	LS F D	

**Figure 8**

pGHV-gpB DNA AF118399 DNA.txt	AATCTTCGTA TCAGAATAAA TAACATTITG GAAGATTTGT CAAAGGCATG -----	50
pGHV-gpB DNA AF118399 DNA.txt	GTTGTCGTGAG CAGCATAGAG CTGCTCTGGT GTGGAATGAG CTCAGCAAGA -----	100
pGHV-gpB DNA AF118399 DNA.txt	TTAACATCCCAC AAGCGTCATG AGCATGATTT ACAATAGACC CGTATCAGCC -----	150
pGHV-gpB DNA AF118399 DNA.txt	AAAAGAATAG GAGATGTCAT TTCAGTCTCT AACTGTATTG TGGTAGACCA -----	200
pGHV-gpB DNA AF118399 DNA.txt	AACCAGTGTC TCATTACATA AAAGTCTCAG GCTTCTCAGT GCATCGGATG -----	250
pGHV-gpB DNA AF118399 DNA.txt	AAAAGTGCTT CTCTAGACCT CCAGTGACAT TAAAGTTAT GAATGACAGT -----	300
	----- TAAT CTATGTCACT T AT ATG CA T	14
pGHV-gpB DNA AF118399 DNA.txt	ACTATTTACA AAGGGCAACT AGGA-GTCAA TAATGAGATT CTCTTAACCA -CTACCC-TA ATCCATCATG AAGACCTGCA TAAATATCCT CAATTAAGG CTA A A A GA T A TAA A T A TTAA	349 62
pGHV-gpB DNA AF118399 DNA.txt	CAACATACCT TGAAACATGT CAGGAAAACA CTGAGTATTA CTTTCAGGCA AGGAGGATTA TGAAACAT----- TTT----- A TGAAACAT TTT	399 83
pGHV-gpB DNA AF118399 DNA.txt	AAGACAGACA TGTACATTTA CAAAAACTAT GAGCATTGAG AGACTGTGCC ----- TG---ATT----- AG---TT----- CTG----- TG ATT AG TT CTG	449 95
pGHV-gpB DNA AF118399 DNA.txt	TTTATCTTCG ATCACCAACAC TAGATACATT TATAGCCCTT AATTTACAC ----- GTCC----- GTCC	499 99
pGHV-gpB DNA AF118399 DNA.txt	TATTGGAGAA TGTTGACTTT -----AAAG TCAT-T-GA A---CTT----- ----- TGTTCACTTT GTAAAAAAAAC ACATATCAGA ATCTCTTCTG TGTT ACTTT AAA CAT T GA A CTT	534 139
pGHV-gpB DNA AF118399 DNA.txt	-----TA----- TAC--CA-- G--GG--ACG AGA----- AG--AGG- TCTAACCTGC TTACAAACATG GCTGGCTAAG AGAAAAATGA TCAGAAAGGA TA TAC CA G GG A G AGA AG AGG	555 189
pGHV-gpB DNA AF118399 DNA.txt	CTTAGTA--A TGT-CT--TT GACA-TTGA- AACAATG----- ATTAGCAGCA TGTGCTGACC CAAAGCTCAG GACAAT-TTT AGATAAACAG TTAG A A TGT CT A A T A ACAAT	585 238
pGHV-gpB DNA AF118399 DNA.txt	----- CAGCTTGCAA TTAAGGTGAC ATGCAATGCT GTGTATGGGT TCACGGTGT -----	585 288
pGHV-gpB DNA AF118399 DNA.txt	----- TGCATCTGGT ATGCTGCCCT GTCTCAAGAT TGCAGAGACC ATAACATATGC -----	585 338
pGHV-gpB DNA AF118399 DNA.txt	----- AAGGAAGGGC CATGTTGGAA AAGACAAAAG TATTTGTAGA GAATTAAAGT -----	585 388
pGHV-gpB DNA AF118399 DNA.txt	----- CATGAGGATC TCCATTCCAT CTGTAAGGTT GGCTTTATGC CTCAGTCACC -----	585 438
pGHV-gpB DNA AF118399 DNA.txt	----- AAACAGCATT GATAAACCT TCAAGGTG 585 ----- 466	

**Figure 9**

pGHV-gpB DNA AF118401 DNA.txt	GAGGACCTGC ATAAGTATCC TCAATTAAAG GAGGATGATT ATGAAACATT	50
pGHV-gpB DNA AF118401 DNA.txt	-----AATCTTC GTATCAGAAT TTTGATTAGT TCTGGCCCTG TTCACTTTGT AAAAAAACAC ATATCAGAAT AA C TATCAGAAT	17 100
pGHV-gpB DNA AF118401 DNA.txt	AAATAACATT TTGGAAGATT TGTCAAAGGC ATGGTGTGCGT GAGCAGCATA ----C-TC TT----- C T TT	67 105
pGHV-gpB DNA AF118401 DNA.txt	GAGCTGCTCT GGTGTGGAAT GAGCTCAGCA AGATTAATCC CACAAGCGTC ---CTG-TC- -----GAA- ---CTT- -G-----CT CACAA---C CTG TC GAA CT G C CACAA C	117 125
pGHV-gpB DNA AF118401 DNA.txt	ATGAGCATGA TTTACAATAG ACCCGTATCA GCCAAAAGAA -----T-- ATG-GC-TG- -----GCCAAGAGAA AAATGATCAG ATG GC TG T	158 152
pGHV-gpB DNA AF118401 DNA.txt	--AGG-----AG-ATGT-----CA --TTT----- AAAGGAATTG ACAGCATGTG CTGATCCAAA GCTCAGGACA ATTTTAGATA AGG AG ATGT CA TTT	172 202
pGHV-gpB DNA AF118401 DNA.txt	-----CAGTC T-----CTA--- ---AC-TGTA TTG-TG-GTA --GA-CCA-- AACAGCAGCT TGCAATTAAG GTGACATGCA ATGCTGTGTA TGGATTCACT CAG T TA AC TG A TG TG GTA GA CA	200 252
pGHV-gpB DNA AF118401 DNA.txt	-----A-----AC-CA G---TGTCTC A-----TTAC GGTGTGCAT CTGGTATGCT GCCATGTCTC AAGATTGCAG AGACCATCAC A A C G TGTCTC A TCAC	217 302
pGHV-gpB DNA AF118401 DNA.txt	-----AT AAAAGT--CT -CAG-GCTTC TATGCAAGGA AGGCCATGT TGGAAAAGAC AAAAGTATTT GTAGAGAAC A AAAAGT T AG G TC	235 352
pGHV-gpB DNA AF118401 DNA.txt	TCAG---TGC A---TCGGA T-GAAAAGT- -GCTT--CTC TAGACCTCCA TGAGTCATGA AGATCTCCGT TCCATATGTA AGGTTGGCTC TATACCTC-A T AG TG A TC G T A A GT G TT CTC TA ACCTC A	273 401
pGHV-gpB DNA AF118401 DNA.txt	GTGACATTAA GTTTATGAA TGACAGTACT ATTTACAAAG GGCAACTAGG GT--CA-TCA A---ACG-- TG-----TTT----- GT CA T A A A G TG TTT	323 417
pGHV-gpB DNA AF118401 DNA.txt	AGTCAATAAT GAGATTCTCT TAACCACAAAC ATACCTGAA ACATGTCAGG -G---ATAAA ----- G ATAA	373 423
pGHV-gpB DNA AF118401 DNA.txt	AAAACACTGA GTATTACTTT CAGGCAAAGA CAGACATGTA CATTACAAA -----	423 423
pGHV-gpB DNA AF118401 DNA.txt	AACTATGAGC ATTTGAAGAC TGTGCCTTTA TCTTCGATCA CCACACTAGA -----	473 423
pGHV-gpB DNA AF118401 DNA.txt	TACATTATA GCCCTTAATT TTACACTATT GGAGAATGTT GACTTTAAAG -----	523 423
pGHV-gpB DNA AF118401 DNA.txt	TCATTGAACT TTATACCAGG GACGAGAAGA GGCTTAGTAA TGTCTTGAC -----	573 423
pGHV-gpB DNA AF118401 DNA.txt	ATTGAAACAA TG 585 ----- 423	

**Figure 10**

```
Query:      1970  aagtcatgtactttataccagggacgagaagaggcttagtaatgtcttgacattgaaa 2029
           ||||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      18669 aagtaatagaactatactctagagaagagaagaggatgagcactgcattgtatagaga 18728
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Query:      2030  caatgttttagggaaataactactatgctcagagggtcagtggcctcagaaaggattgc 2089
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      18729 ccatgttttagagaatacaactactacacacagagggtcactggcctgcggagggacttga 18788
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Query:      2090  tggatctaaggccaatagaatcaatttgtggatgcatttgttagtcttatggatgatt 2149
           || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      18789 cagacctagctacaacacagaatcaatttgttagatgccttgtgacgcctcatggacgact 18848
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Query:      2150  tgggtgtctgttgggcagacagttgtaaatgctgttaagtgggtggctacgctgttagct 2209
           || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      18849 tgggggtcggtggggaaaacggtgttgaatgctgtgagcagtgtagggccacactcttcagct 18908
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Query:      2210  caattgttaacaggatttattatcaaattttcataaaaaccatttgttggaatgtt 2261
           || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      18909 ctatagtctcaggatcatcaattttcataaaaaccctttggggaatgtt 18960
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Score = 91.1 bits (47), Expect = 7e-16
Identities = 117/152 (76%), Positives = 117/152 (76%)
  
  

Query:      1498  tgggtgtcggtggccatagagctgctctgggtgttggaaatgagctcagcaagattaatccc 1557
           || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      18194 tgggtgccgtggccatagagctcaccggcgttcatgttggaaacgagctaaggcaaaatcaaccct 18253
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Query:      1558  acaaggcgtcatgagcatgatttacaatagaccgtatcagccaaaagaataggagatgtc 1617
           || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      18254 accagtgtgtatgagctctatatacggccggccagtatctgcctaaaagaatggagatgtg 18313
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Query:      1618  atttcagtcacttactgttatttgttggtagacca 1649
           || | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      18314 atatctgtctctactgtgttgtggatgacca 18345
```

**Figure 11(a)**

gi|2337975 (AF005370) glycoprotein B [Alcelaphine herpesvirus 1]  
Length = 854

Score = 953 bits (2437), Expect = 0.0  
Identities = 463/804 (57%), Positives = 589/804 (72%), Gaps = 26/804 (3%)

Query: 74 KNIYGSPSTFPYRVCASAGVGDVFRFQTDHVCPDASDMVHSEGILLIYKQNIIPFMFRVR 133  
K I+ PS FP+RVCAS +GD+FRFQT H CP+ D H+EGILLI+K+NI+P++F+VR  
Sbjct: 55 KGIHSFPSAFPPRVCASASNIGDIFRFQTSHPNTKDKHENEGILLIFKENIVPYVFKVR 114

Query: 134 KYRKVVTTSTVYNGIYSDSITNQHTFYKSIEPWETEKMDTIYQCFNSRLNNTGGNLLTYV 193  
KYRK+VTTST+YNGIY+D++TNQH F KS+ +ET +MDTIYQC+NSL + GGNLL Y  
Sbjct: 115 KYRKIVTTSTIYNGIYADAVTNQHVFSKSVPIYETRRMDTIYQCYNSLDVTVGGNLLVYT 174

Query: 194 DRDDINMTVFLQPVDGVTPDVKRYGSQPELYLEPGFWGFSYRRRTTVNCLEMDFARSNP 253  
D D NMTV LQPVDG++ V+RY SQPE++ EPGW G YRRRTTVNCE+ + AR+ P  
Sbjct: 175 DNDGSNMTVDLQPVDGLSNVRRYHSQPEIHAEPGWLLGGYRRRTVNCEVTETDARAVP 234

Query: 254 PFDFVFTATGDTVEMSPFWSGEDDHENKMHEKPWFVSVINNYKVVVDYQNRGTVPLGKTRI 313  
PF +F+T GDT+EMSPFW + E + +V +Y+VVDY+ RGT P G TRI  
Sbjct: 235 PFRYFITNIGDTIEMSPFWSKAWNTEFSGEPDRTLTVAKDYRVVDYKFRGTQPQGHTRI 294

Query: 314 FLDREETYTLSWEKHLKNMSYCPLTLWKAFYNGIQTEHSGSYHFVANDITASFTTSKEDMK 373  
F+D+EETYLSW + +N+SYC WK+F N I+TEH S HFVANDITASF T +  
Sbjct: 295 FVDKEEYTLSWAQQFRNISYCRWAHWKSFDNAIKTEHGKSLHFVANDITASYTPNTQTR 354

Query: 374 EFNTTYHCLNXXXXXXXXXXXXXVNSTHSKYGDLKYFKTDGGLYLVWQPLIQNRLDAKN 433  
E + CLN VN THS G +Y+ T+GGL LVWQPL+Q +LLDAK  
Sbjct: 355 EVLGKHVCLNNNTIESELKSRLAKVNDTHSPNGTAQYYLTNGGLLWWQPLVQQKLDAKG 414

Query: 434 KLN-----NETYSRRSRRQAESTTDPMMEMTGNGAGGEYSSSENSITVAQVQYAYDN 484  
L+ T + RSRRQ S + +G Y++E++I + Q+Q+AYD  
Sbjct: 415 LLDAVKKQQNTTTTTTRSRQRQRSVS-----SGIDDVYTAESTILLTQIQFAYDT 466

Query: 485 LRIRINNILEDLSKAWCREQHRAALVWNELSKINPTSVMMSMIYNRPVSAKRIGDVISVS 544  
LR +INN+LE+LS+AWCREQHRA+L+WNELSKINPTSVMMS IY RPVSAKRIGDVISVS+  
Sbjct: 467 LRAQINNVLEELSRAWCREQHRASLMWNELSKINPTSVMSSIYGRPVSAKRIGDVISVSH 526

Query: 545 CIVVDQTSVSLHKSLLSA-SDEKCFSPRPFKFMNDSTIYKGQLGVNNEILLTTYL 603  
C+VVDQ SVSLH+S+R+ +C+SRPPVTFKF+NDS +YKGQLGVNNEILLTTT +  
Sbjct: 527 CVVVDQDSVSLHRSMRVPGRDKTHECYSRPPVTFKFINDSHLYKGQLGVNNEILLTTAV 586

Query: 604 ETCQENTEYYFQAKTDMYIYKNYEHLKTVPLSSITTLDTFIALNFTLLENVDFKVIELYT 663  
E C ENTE+YFQ +MY YKNY H+KT+P+ + TLDTF+ LN TL+EN+DF+VIELYT+  
Sbjct: 587 EICHENTEHYFQGGNNMYFYKNYRHVKTMMPVGDVATLDTFMVLNLVENIDFQVIELYS 646

Query: 664 RDEKRLSNVFDIETMFREYNYYAQRVSGLRKDLLDLSTNRNQFVDAFGSLMDDLGAVGQT 723  
R+EKR+S FDIETMFREYNYY QRV+GLR+DL DL+TNRNQFVDAFGSLMDDLG VG+T  
Sbjct: 647 REEKRMSTAFDIETMFREYNYYTQRVTGLRRDLTDLATNRNQFVDAFGSLMDDLGAVGKT 706

**Figure 11(b)**

Query: 724 VVNAVSGVATLFSSIVTGFINFIFKNPFGGMLMIVVIGVLFAIYFLTKKTKIYETAPIKM 783  
V+NAVS VATLFSSIV+G INFIFKNPFGGML+ ++ V+ + L +K K + P++M  
Sbjct: 707 VLNAVSSVATLFSSIVSGIINFIFKNPFGGMLLFGLIAAVVITVILLNRKAKRFAQNPVQM 766

Query: 784 IYPEIDKLKEREKGKSEIAPISEEEELERIVLAMHIHQQNShMETK-----TRKDPKDSI 836  
IYP+I + + + + PIS+ EL+RI+LAMH + + E+K T P D  
Sbjct: 767 IYPDIKTITSQREELQVDPISKHELDRLIMLAMHDYHASKQPESKQDEEQGSTTSGPAD-W 825

Query: 837 LTRAQNMLRKRSGYSNLKNAESVE 860  
L +A+N+LR+R+GY LK +S E  
Sbjct: 826 LNKAKNVLRRAGYKPLKRTDSFE 849